

SEQUENCE LISTING

<110> Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME

<130> COP_TEXT.DOC

<160> 28

<170> PatentIn version 3.1

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<211> 1010

<212> DNA

<213> Pontellina plumata

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<212> PRT

<213> Pontellina plumata

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Val Val Phe Glu Leu Val Gly Gly Gly Glu Gly Ile Pro Glu Gln Gly
20           25           30
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Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
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 210 215 220

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<211> 1010

<212> DNA

<213> *Pontellina plumata*

<400> 3

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 ctcttgagca gggacgtatg accaacaaga tgaagtctac caagggcgcc ttgaccttct 180
 cccctacct tctctctcat gtcattgggat acgggttcta ccactttggt acctatccca 240
 gtgggtatga gaatcccttc ctgcatgcca tcaacaacgg ggggtacacc aacaccagga 300
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 tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttgcaccca atgggagaca 480
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<210> 4

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<212> PRT

<213> Pontellina plumata

<400> 4

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Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
          145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205

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Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
 210 215 220

<210> 5
 <211> 814
 <212> DNA
 <213> Labidocera aestiva
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gatggaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaa aggacctctc      180
tccttctctc cctacctact ctccacatc atgggctacg gattctatca ctatgctacc      240
ttccctgctg gatatgagaa tgtctacctc catgctgcta agaatggagg ctacaccaac      300
accaggactg agaggtacga agacggagga atcatttcgg tcaacttcac ctacagatat      360
gagggaaaca aggttatcgg agacttcaag gttgttggtat caggattccc agctaacagt      420
gttatcttca ctgacaagat catcaagtcc aaccaaacct gtgagcacat ctacccaag      480
ggagataata ttcttgtcaa tgctacact cgaacttgga tgctgagaga tgggtggatac      540
tactctgcac aggtcaacaa tcctctccac ttcaagactg ccatgcatcc caccatgctc      600
cagaacggag gatccatgtt tacctacagg aaggttgagg agctccacag ccagtcagat      660
gttggtattg tagaatacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg      720
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<210> 6
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Met Pro Val Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala
          50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn
65           70           75           80

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Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
 130 135 140
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe
 165 170 175
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 7
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 <212> DNA
 <213> cf. Pontella meadi Wheeler
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 ctccctacct cctctccac attcttggt acggatatta ccaactttgca accttccctg 240
 ctggatatga aaatatctac cttcatgcc tgaagaatgg aggttactcc aatgtcagaa 300
 ctgagaggta tgaggatgga ggcacatctt ctataacctt caactacaga tatgaaggga 360
 acaagatcat tggagacttc aagggttggt gaacaggatt ccctaccaac agtcttatct 420
 tcaactgaaa gatcattaaa tccaacctta cctgtgagaa catgttcccc aaggctgaca 480
 atactcttgt gaatgcctac accagaacat atttgcttaa agatggtgga tactactctg 540
 cccagggtta caaccatag cacttcaaga gtgccatcca taccaccatg ctccagaatg 600
 gcggatccat gttcacctac agagttgtag aggagacaca cactcagaac gaagttgcta 660
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 aaactgcaaa gaaataaact aaattgtaca atc 753

<210> 8
 <211> 222

<212> PRT

<213> cf. *Pontella meadi* Wheeler

<400> 8

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Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Ile Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
20           25           30
Arg Met Thr Asn Lys Met Lys Ser Ile Lys Gly Pro Ile Ser Phe Ser
35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Asn Lys Ile Ile Gly
100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Thr Asn Ser Leu Ile Phe
115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
130          135          140
Lys Ala Asp Asn Thr Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145          150          155          160
Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
165          170          175
Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe
180          185          190
Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile
195          200          205
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
210          215          220

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<210> 9

<211> 880

<212> DNA

<213> cf. *Pontella meadi* Wheeler

<400> 9

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agtccatcaa aggacctctc tccttctctc cctacctact ctcccacatt cttggctatg 300
gatattacca ctttgcaacc ttccctgctg gatatgaaaa tatctacctt catgccatga 360
agaatggagg ttactcaaat gtcaggactg agaggatga ggatggaggc atcatttcta 420
taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa 480
caggattccc taccgacagt cttatcttca ctgacaagat cattaaatcc aaccctacct 540
gcgagaacat gttccccaag gctgacaaca ttcttgtgaa tgcctacacc agaacctatt 600
tgcttaaaga tgggtggatac tactctgccc aggttaacaa ccatatgcac ttcaagagtg 660
ccatccatcc tacaatgctc cagaatggtg gatccatggt cactcacaga gtagtagagg 720
agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta 780
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<210> 10

<211> 222

<212> PRT

<213> cf. *Pontella meadi* Wheeler

<400> 10

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Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly
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Glu Glu Phe Glu Leu Ile Gly Ser Gly Asp Gly Asn Thr Asp Gln Gly
          20           25           30
Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
          50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
          85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly
          100          105          110
Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
          130          135          140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145          150          155          160

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Lys	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Phe
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Lys	Ser	Ala	Ile	His	Pro	Thr	Met	Leu	Gln	Asn	Gly	Gly	Ser	Met	Phe
				180				185				190			
Thr	His	Arg	Val	Val	Glu	Glu	Asn	His	Thr	Lys	Thr	Asn	Val	Ala	Ile
				195				200				205			
Val	Glu	Tyr	Gln	Asn	Val	Phe	Lys	Thr	Pro	Thr	Ala	Phe	Ala		
				210				215				220			

<210>	11
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<212>	DNA
<213>	Pontella mediterranea
<400>	11

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tttgaacttg	ttggtgctgg	agaaggaaac	actgatgagg	gacgcatgac	caacaagatg	180
aagtccacca	agggacctct	ttccttctct	cottatttgc	tctccacgt	tcttggttat	240
ggatactacc	actatgctac	cttccctgct	ggatatgaaa	atgtctacct	ccatgccatg	300
agaatggag	gttactcaa	cacaagaact	gagaggtatg	aggatggagg	tatcatttct	360
gctaccttca	actacagata	tgaagggaga	cagattcatg	gagacttcaa	ggttgtagga	420
acgggattcc	ctgccgacag	catcatcttc	actgacaaga	tcatcaagtc	caaccctacc	480
tgtgagcaca	tctaccccaa	ggctaacaat	attcttgtga	atgcttacac	cagaacctgg	540
atgcttagag	atggtggata	ctactctgcc	cagggtcaaca	accacatgca	tttacagagt	600
gccattcatc	ccaccatgct	caagaatggg	ggatctatgt	tcacctacag	aaaggttgag	660
gagctccaca	cacaaactga	agtcgggtatt	gttgaatacc	agcatgtctt	caagaggcca	720
actgcttttg	cttaattttg	taaataaaga	aagaatctat	aatgcaatag	taccttaaag	780
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aaaaaaa						847

<210>	12
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<212>	PRT
<213>	Pontella mediterranea
<400>	12

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Glu	Glu	Phe	Glu	Leu	Val	Gly	Ala	Gly	Glu	Gly	Asn	Thr	Asp	Glu	Gly
			20					25					30		

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
 50 55 60
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
 65 70 75 80
 Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
 130 135 140
 Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu
 165 170 175
 Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
 210 215 220

<210> 13
 <211> 850
 <212> DNA
 <213> *Pontella mediterranea*
 <400> 13

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 tttgaacttg ttgggtgctgg agatggaaac actgatgagg gacgcatgac caaccagatg 180
 aagtccacaa agggacctct ctcttctctt ccctacttgc tctccacgt tcttggtctat 240
 ggatactacc actatgctac cttccctgct ggatatgaaa atgtctacct ccatgccatg 300
 aagaatggag gttactccaa cacaagaact gagaggtatg acgatggagg tatcatttct 360
 gctaccttca actacagata tgaagggaga cagattcatg gagacttcaa gggtgttgga 420
 actggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caaccctacc 480
 tgtgagcaca tctaccccaa ggctgacaat attcttgtga atgcctacac cagaacctgg 540
 atgcttagag atgggtggata ctactctgct cagggtcaaca accacatgca ctttaagagt 600

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gccatccatc ccaccatgct ccagaatggt ggatctatgt tcacctacag aaagggttgag      660
gagctccaca cacaaactga agttgggtatt gttgagtacc agcatgtttt caagaggccc      720
acagcttttg ctttaattttg taaataaaga aagaatttat aatacaatag tgcttttatg      780
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aaaaaaaaaa                                850

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<210> 14

<211> 222

<212> PRT

<213> *Pontella mediterranea*

<400> 14

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Met Pro His Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
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Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
              20              25              30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
              35              40              45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
              50              55              60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65              70              75              80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
              85              90              95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
              100             105             110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
              115             120             125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
              130             135             140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145             150             155             160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
              165             170             175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
              180             185             190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
              195             200             205
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
              210             215             220

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<210> 15
 <211> 821
 <212> DNA
 <213> Unknown
 <220>
 <223> nucleic acid sequence for pdaelGFP from an unidentified
 Pontellidae species, complete cds
 <400> 15

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ggaaatactg atcagggacg tatgaccaac aagatgaaat ctaccaaggg tccactctcc    180
ttctctccct atcttctctc tcatgtcatg ggatatggat tctatcattt tggaacattt    240
cccagtgggt atgagaatcc ctatgtccac gccatgacga acggtggata taccaacacc    300
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atcttcactg acaagatcat caagtccaac cccaattgtg aacatttcta tccaatggct    480
gaaaacatca tgaaaaatgc ctacatgaga actctctccc tcagagatgg tggctactac    540
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<210> 16
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 <213> Unknown
 <220>
 <223> amino acid sequence for pdaelGFP from an unidentified Pontellidae
 species
 <400> 16

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Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
  
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Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly
 100 105 110
 Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro
 130 135 140
 Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe
 165 170 175
 Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 17

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the humanized version of the ppluGFP2

<400> 17

atgcccgcca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag 60
 ctgggtggg cgaggagagg caccgccgag cagggccgca tgaccaacaa gatgaagagc 120
 accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc 180
 taccacttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240
 ggcggtctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
 ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc 360
 ttccccgagg acagcgtgat cttcacggac aagatcatcc gcagcaacgc caccgtggag 420
 cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg 480
 cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc 540
 caccacagca tcctgcagaa cggggggccc atgttcgcct tccgccgcgt ggaggagctg 600
 cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca 660
 ttcgcctga 669

Met	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn	Gly
1				5				10				15			
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
20				25				30							
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
35				40				45							
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
50				55				60							
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
65				70				75				80			
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
85				90				95							
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
100				105				110							
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
115				120				125							
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
130				135				140							
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
145				150				155				160			
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
165				170				175							
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Pro	Met	Phe
180				185				190							
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
195				200				205							
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala		
210				215				220							

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<210> 19
<211> 589
<212> DNA
<213> Artificial sequence
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<220>

<223> nucleic acid sequence for the ppluGFP2 with yeast-optimized codon usage

<400> 19

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tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt      60
ttctccatat ttgttgtctc atgttatggg ttatgggtttt tatcattttg gtacttatcc      120
atctgggttat gaaaatccat ttttgcattgc tattaataat ggtgggttata ctaataactag      180
aattgaaaaa tatgaagatg gtgggtgtttt gcatgtttct ttttcttata gatatgaagc      240
tggtagagtt attggcgatt ttaaagttgt tggtactggg tttccagaag attctgttat      300
ttttactgat aaaattatta gatctaatac tactgttgaa catttgcatt caatgggtga      360
taatgttttg gttgggttctt ttgctagaac tttttctttg agagatgggtg gttattattc      420
ttttgttggt gattctcata tgcattttta atctgctatt catccatcta ttttgcaaaa      480
tggtgggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg      540
tattgttgaa tatcaacatg cttttaaaac tccaattgct tttgcttaa      589
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<210> 20

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the ppluGFP2 with yeast-optimized codon usage

<400> 20

```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115          120          125
```

Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
 210 215 220

<210> 21
 <211> 669
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> nucleic acid sequence for the CopCFP mutant
 <400> 21

atgcccgccca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag 60
 ctggtgggcg gcggagaggg caccgccgag cagggccgca tga'ccaaca gatgaagagc 120
 accaaaggcg cctgacctt cagcccctac ctgctgagcc acgtgatggg ctggggcttt 180
 taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240
 ggcggtctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
 ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc 360
 ttccccgagg acagcgtgat cttaccgcac aagatcatcc gcagcaacgc caccgtggag 420
 cacctgcgcc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg 480
 cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcaacttcaa gagcgccatc 540
 caccacagca tcctgcagaa cgggggcccc atgttcgcct tcgcccgcgt ggaggagctg 600
 cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca 660
 ttgcgctaa 669

<210> 22
 <211> 222
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> amino acid sequence for the CopCFP mutant
 <400> 22

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
 1 5 10 15
 Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
 20 25 30
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 23

<211> 690

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA1 variant

<400> 23

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc 60
 ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc 120
 atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc 180
 cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc 240


```

ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcatcgagaa gtacgaggac   300
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac   360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc   420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc   480
ttcgcccgcg ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac   540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc   600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac   660
gccttcaaga ccccgatcgc attcgctga                                     690

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<210> 24

<211> 229

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA1 variant

<400> 24

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Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1           5           10           15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
          20           25           30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
          35           40           45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
          50           55           60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65           70           75           80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
          85           90           95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
          100          105          110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
          115          120          125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
          130          135          140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145          150          155          160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
          165          170          175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
          180          185          190

```

Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
 195 200 205
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
 210 215 220

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

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atgcccgccca tgaagatcga gtgccgcatac accggcacccc tgaacggcgt ggagttcgag      60
ctggtggggcg gcggagaggg cacccccgag cagggccgca tgaccaacaa gatgaagagc      120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc      180
taccacttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac      240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc      300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcacccggc      360
ttccccgagg acagcgtgat cttcacccgac aagatcatcc gcagcaacgc caccgtggag      420
cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcaactcaa gagcgccatc      540
caccccagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca      660
ttcgccagat ccagagccca ggccagcaac tccgccgtgg atggcacagc cggaccggga      720
tcggccgcga ctctagatca taatcagcca taccacattt gtagaggttt tacttgcttt      780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa      819

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<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
 1 5 10 15

Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
 20 25 30
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser
 210 215 220
 Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly
 225 230 235 240
 Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly
 245 250 255
 Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
 260 265 270

<210> 27

<211> 840

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA3 variant

<400> 27

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc

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ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc 120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc 180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc 240
ttcctgcacg ccatcaacaa cggcggctac accaacaccc gcatcgagaa gtacgaggac 300
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac 360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc 480
ttcggccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attcgccaga tccagagccc aggccagcaa ctccgccgtg 720
gatggcacag ccggaccggg atcgccgcg actctagatc ataatcagcc ataccacatt 780
tgtagagggt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaaacataa 840

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<210> 28

<211> 279

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA3 variant

<400> 28

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Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1           5           10          15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
          20          25          30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
          35          40          45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
          50          55          60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65          70          75          80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
          85          90          95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
          100         105         110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
          115         120         125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
          130         135         140

```

Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145 150 155 160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
165 170 175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
180 185 190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
195 200 205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
210 215 220
Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
225 230 235 240
Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
245 250 255
Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr
260 265 270
Pro Pro Pro Glu Pro Glu Thr
275